The listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently amended) A method for amplifying expressed genetic sequences from genomic DNA (gDNA) selected from a higher-order eukaryotic species, for printing on DNA microarrays, wherein the method comprises:

identifying a 3' untranslated region (3'UTR) of a gDNA sequence based on the presence of a stop codon and a polyadenylation signal in the gDNA sequence;

selecting a predetermined gDNA sequence within the 3'UTR;

designing a probe for said predetermined gDNA sequence;

performing a first polymerase chain reaction (PCR) with the probe for the ~~3'UTR on~~ predetermined gDNA sequence within the 3'UTR to generate a first PCR-product having the amplified gDNA sequence;

separating the resulting first PCR-product by a size-differentiation process selected from the group consisting of electrophoresis and chromatography;

selecting a predetermined band from the size-differentiated samples;

performing a second polymerase chain reaction with the probe to amplify the selected predetermined band within the 3'UTR to generate a second PCR product; and

printing the second PCR product on a substrate to form an array, wherein the printed product is free of ~~polyadenosine sequences~~ a polyA tail.

2. – 3. (Cancel)

4. (Previously presented) The method according to claim 1, wherein said predetermined gDNA sequence within the 3'UTR is selected by use of computer software.

5. (Previously presented) The method according to claim 1, wherein said selected predetermined gDNA sequence within the 3'UTR has a length of at least about 75 nucleotides.

6. (Original) The method according to claim 5, wherein said selected predetermined gDNA sequence has a length of about 200 to about 600 bases.

7. (Original) The method according to claim 6, wherein said selected predetermined gDNA sequence has a length of about 250 to about 450 bases.

8. (Original) The method according to claim 1, wherein said selected predetermined gDNA sequence has an overall homology of less than or equal to about 70% to any other genomic sequence in the same genome.

9. (Original) The method according to claim 8, wherein said selected predetermined gDNA sequence has an overall homology of less than or equal to about 40% to any other genomic sequence in the same genome.

10. (Original) The method according to claim 8, wherein said selected predetermined gDNA sequence has an overall homology of from about 20% to 30% to any other genomic sequence in the same genome.

11. (Previously amended) The method according to claim 1, wherein the printed product contains over 90 percent correct predetermined sequence.

12. (Previously presented) The method according to claim 1, wherein said array has a rectilinear format.

13.-26. (Cancelled)

27. (Previously presented) The method according to claim 1, wherein said predetermined gDNA sequence within the 3'UTR has a length of up to about 2000 nucleotides.

28. (Currently amended) A method for amplifying expressed genetic sequences from genomic DNA (gDNA) selected from a higher-order eukaryotic species, for printing on DNA microarrays, wherein the method comprises:

identifying an exon of a gene defined by computer software;

selecting a predetermined gDNA sequence within the exon;

designing a probe for said predetermined gDNA sequence;

performing a first polymerase chain reaction (PCR) with the probe for the ~~exon on~~ predetermined gDNA sequence within the exon to generate a first PCR-product having the amplified gDNA sequence;

separating the first PCR-product by a size-differentiation process selected from the group consisting of electrophoresis and chromatography;

selecting a predetermined band from the size-differentiated samples;

performing a second PCR with the probe to amplify a product in the predetermined band; and

printing the product of the second PCR of the amplified predetermined band on a substrate to form an array.

29. (Withdrawn) A method for making a DNA array, comprising:

performing a first PCR to amplify a 3'UTR, or a segment thereof, in a gDNA of a higher-order eukaryotic species;

separating products of said first PCR to select a product with a predetermined size;

performing a second PCR to amplify a sequence in said selected product; and

depositing said amplified sequence to a substrate of the DNA array.

30. (Withdrawn) The method of claim 29, comprising:

performing PCRs to amply a plurality of 3'UTRs, or segments thereof, in genomic DNAs of said higher-order eukaryotic species;

separating products of said PCRs to select products with predetermined sizes;

performing PCRs to amplify sequences in said selected products; and

depositing said amplified sequences to the DNA array.

31. (Withdrawn) The method of claim 30, wherein each said 3'UTR is located between a stop codon and a polyadenylation signal of a different respective gene.

32. (Withdrawn) The method of claim 31, wherein each said 3'UTR or segment comprises from about 75 to about 2,000 nucleotides, and each said separating step is accomplished by electrophoresis or chromatography.

33. (Withdrawn) The method of claim 31, wherein said higher-order eukaryotic species is a mammal, and each said 3'UTR or segment has an overall homology of no more than about 40% to any other genomic sequence in the genome of said mammal.

34. (Withdrawn) The method of claim 29, wherein said first and second PCRs are performed using the same pair of primers.